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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/393,795

DATE: 12/02/1999
TIME: 18:41:58

Input Set: I393795.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

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1  <110> APPLICANT: Gray, John T.
2      Mulligan, Richard C.
3  <120> TITLE OF INVENTION: Packaging Cell Lines
4  <130> FILE REFERENCE: CMCC693p2A
5  <140> CURRENT APPLICATION NUMBER: US/09/393,795
6  <141> CURRENT FILING DATE: 1999-09-10
7  <150> EARLIER APPLICATION NUMBER: US 60/100,063
8  <151> EARLIER FILING DATE: 1998-09-12
9  <150> EARLIER APPLICATION NUMBER: US 60/100,022
10 <151> EARLIER FILING DATE: 1998-09-11
11 <160> NUMBER OF SEQ ID NOS: 12
12 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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14 <211> LENGTH: 396
15 <212> TYPE: DNA
16 <213> ORGANISM: Homo sapien
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19      ttaaggccag ggggaaagaa aaaatataaa ttaaaacata tagtatgggc aagcagggag      120
20      ctagaacgat tcgcagttaa tcctggcctg ttagaaacat cagaaggctg tagacaaata      180
21      ctgggacagc tacaaccatc ccttcagaca ggatcagaag aacttagatc attatataat      240
22      acagtagcaa ccctctattg tgtgcatcaa aggatagaga taaaagacac caaggaagct      300
23      ttagacaaga tagaggaaga gcaaaacaaa agtaagaaaa aagcacagca agcagcagct      360
24      gacacaggac acagcaatca ggtcagccaa aattac      396
25 <210> SEQ ID NO 2
26 <211> LENGTH: 1503
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapien
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)...(1503)
32 <400> SEQUENCE: 2
33      atg ggt gcg aga gcg tcg gta tta agc ggg gga gaa tta gat aaa tgg      48
34      Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Lys Trp
35      1          5          10          15
36      gaa aaa att cgg tta agg cca ggg gga aag aaa caa tat aaa cta aaa      96
37      Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Gln Tyr Lys Leu Lys
38      20          25          30
39      cat ata gta tgg gca agc agg gag cta gaa cga ttc gca gtt aat cct      144
40      His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
41      35          40          45
42      ggc ctt tta gag aca tca gaa ggc tgt aga caa ata ctg gga cag cta      192
43      Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
44      50          55          60

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45	caa cca tcc ctt cag aca gga tca gaa gaa ctt aga tca tta tat aat	240
46	Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn	
47	65 70 75 80	
48	aca ata gca gtc ctc tat tgt gtg cat caa agg ata gat gta aaa gac	288
49	Thr Ile Ala Val Leu Tyr Cys Val His Gln Arg Ile Asp Val Lys Asp	
50	85 90 95	
51	acc aag gaa gcc tta gat aag ata gag gaa gag caa aac aaa agt aag	336
52	Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys	
53	100 105 110	
54	aaa aag gca cag caa gca gca gct gac aca gga aac aac agc cag gtc	384
55	Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly Asn Asn Ser Gln Val	
56	115 120 125	
57	agc caa aat tac cct ata gtg cag aac ctc cag ggg caa atg gta cat	432
58	Ser Gln Asn Tyr Pro Ile Val Gln Asn Leu Gln Gly Gln Met Val His	
59	130 135 140	
60	cag gcc ata tca cct aga act tta aat gca tgg gta aaa gta gta gaa	480
61	Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu	
62	145 150 155 160	
63	gag aag gct ttc agc cca gaa gta ata ccc atg ttt tca gca tta tca	528
64	Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser	
65	165 170 175	
66	gaa gga gcc acc cca caa gat tta aat acc atg cta aac aca gtg ggg	576
67	Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly	
68	180 185 190	
69	gga cat caa gca gcc atg caa atg tta aaa gag acc atc aat gag gaa	624
70	Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu	
71	195 200 205	
72	gct gca gaa tgg gat aga ttg cat cca gtg cat gca ggg cct att gca	672
73	Ala Ala Glu Trp Asp Arg Leu His Pro Val His Ala Gly Pro Ile Ala	
74	210 215 220	
75	cca ggc cag atg aga gaa cca agg gga agt gac ata gca gga act act	720
76	Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr	
77	225 230 235 240	
78	agt acc ctt cag gaa caa ata gga tgg atg aca cat aat cca cct atc	768
79	Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr His Asn Pro Pro Ile	
80	245 250 255	
81	cca gta gga gaa atc tat aaa aga tgg ata atc ctg gga tta aat aaa	816
82	Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys	
83	260 265 270	
84	ata gta aga atg tat agc cct acc agc att ctg gac ata aga caa gga	864
85	Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly	
86	275 280 285	
87	cca aag gaa ccc ttt aga gac tat gta gac cga ttc tat aaa act cta	912
88	Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu	
89	290 295 300	
90	aga gcc gag caa gct tca caa gag gta aaa aat tgg atg aca gaa acc	960
91	Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr	
92	305 310 315 320	
93	ttg ttg gtc caa aat gcg aac cca gat tgt aag act att tta aaa gca	1008
94	Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala	

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95          325          330          335
96      ttg gga cca gga gcg aca cta gaa gaa atg atg aca gca tgt cag gga      1056
97      Leu Gly Pro Gly Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly
98          340          345          350
99      gtg ggg gga ccc ggc cat aaa gca aga gtt ttg gct gaa gca atg agc      1104
100     Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser
101          355          360          365
102     caa gta aca aat cca gct acc ata atg ata cag aaa ggc aat ttt agg      1152
103     Gln Val Thr Asn Pro Ala Thr Ile Met Ile Gln Lys Gly Asn Phe Arg
104          370          375          380
105     aac caa aga aag act gtt aag tgt ttc aat tgt ggc aaa gaa ggg cac      1200
106     Asn Gln Arg Lys Thr Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His
107     385          390          395          400
108     ata gcc aaa aat tgc agg gcc cct agg aaa aag ggc tgt tgg aaa tgt      1248
109     Ile Ala Lys Asn Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys
110          405          410          415
111     gga aag gaa gga cac caa atg aaa gat tgt act gag aga cag gct aat      1296
112     Gly Lys Glu Gly His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn
113          420          425          430
114     ttt tta ggg aag atc tgg cct tcc cac aag gga agg cca ggg aat ttt      1344
115     Phe Leu Gly Lys Ile Trp Pro Ser His Lys Gly Arg Pro Gly Asn Phe
116          435          440          445
117     ctt cag agc aga cca gag cca aca gcc cca cca gaa gag agc ttc agg      1392
118     Leu Gln Ser Arg Pro Glu Pro Thr Ala Pro Pro Glu Glu Ser Phe Arg
119          450          455          460
120     ttt ggg gaa gag aca aca act ccc tct cag aag cag gag ccg ata gac      1440
121     Phe Gly Glu Glu Thr Thr Thr Pro Ser Gln Lys Gln Glu Pro Ile Asp
122     465          470          475          480
123     aag gaa ctg tat cct tta gct tcc ctc aga tca ctc ttt ggc agc gac      1488
124     Lys Glu Leu Tyr Pro Leu Ala Ser Leu Arg Ser Leu Phe Gly Ser Asp
125          485          490          495
126     ccc tcg tca caa taa      1503
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128          500
129     <210> SEQ ID NO 3
130     <211> LENGTH: 500
131     <212> TYPE: PRT
132     <213> ORGANISM: Homo sapien
133     <400> SEQUENCE: 3
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135     1          5          10          15
136     Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Gln Tyr Lys Leu Lys
137     20          25          30
138     His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
139     35          40          45
140     Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
141     50          55          60
142     Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn
143     65          70          75          80
144     Thr Ile Ala Val Leu Tyr Cys Val His Gln Arg Ile Asp Val Lys Asp

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145		85		90		95	
146	Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys						
147		100		105		110	
148	Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly Asn Asn Ser Gln Val						
149		115		120		125	
150	Ser Gln Asn Tyr Pro Ile Val Gln Asn Leu Gln Gly Gln Met Val His						
151		130		135		140	
152	Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu						
153	145		150		155		160
154	Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser						
155		165		170		175	
156	Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly						
157		180		185		190	
158	Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu						
159		195		200		205	
160	Ala Ala Glu Trp Asp Arg Leu His Pro Val His Ala Gly Pro Ile Ala						
161		210		215		220	
162	Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr						
163	225		230		235		240
164	Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr His Asn Pro Pro Ile						
165		245		250		255	
166	Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys						
167		260		265		270	
168	Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly						
169		275		280		285	
170	Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu						
171		290		295		300	
172	Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr						
173	305		310		315		320
174	Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala						
175		325		330		335	
176	Leu Gly Pro Gly Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly						
177		340		345		350	
178	Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser						
179		355		360		365	
180	Gln Val Thr Asn Pro Ala Thr Ile Met Ile Gln Lys Gly Asn Phe Arg						
181		370		375		380	
182	Asn Gln Arg Lys Thr Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His						
183	385		390		395		400
184	Ile Ala Lys Asn Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys						
185		405		410		415	
186	Gly Lys Glu Gly His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn						
187		420		425		430	
188	Phe Leu Gly Lys Ile Trp Pro Ser His Lys Gly Arg Pro Gly Asn Phe						
189		435		440		445	
190	Leu Gln Ser Arg Pro Glu Pro Thr Ala Pro Pro Glu Glu Ser Phe Arg						
191		450		455		460	
192	Phe Gly Glu Glu Thr Thr Thr Pro Ser Gln Lys Gln Glu Pro Ile Asp						
193	465		470		475		480
194	Lys Glu Leu Tyr Pro Leu Ala Ser Leu Arg Ser Leu Phe Gly Ser Asp						

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195		485	490	495	
196	Pro Ser Ser Gln				
197	500				
198	<210> SEQ ID NO 4				
199	<211> LENGTH: 1503				
200	<212> TYPE: DNA				
201	<213> ORGANISM: Artificial Sequence				
202	<220> FEATURE:				
203	<223> OTHER INFORMATION: Codon optimized form of HIV gag coding region				
204	<220> FEATURE:				
205	<221> NAME/KEY: CDS				
206	<222> LOCATION: (1)...(1503)				
207	<400> SEQUENCE: 4				
208	atg ggc gcc cgc gcc tcc gtg ctg tcc ggc ggc gag ctg gac aag tgg				48
209	Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Lys Trp				
210	1 5 10 15				
211	gag aag atc cgc ctg cgc ccc ggc ggc aag aag cag tac aag ctg aag				96
212	Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Gln Tyr Lys Leu Lys				
213	20 25 30				
214	cac atc gtg tgg gcc tcc cgc gag ctg gag cgc ttc gcc gtg aac ccc				144
215	His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro				
216	35 40 45				
217	ggc ctg ctg gag acc tcc gag ggc tgc cgc cag atc ctg ggc cag ctg				192
218	Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu				
219	50 55 60				
220	cag ccc tcc ctg caa acc ggc tcc gag gag ctg cgc tcc ctg tac aac				240
221	Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn				
222	65 70 75 80				
223	acc atc gcc gtg ctg tac tgc gtg cac cag cgc atc gac gtg aag gac				288
224	Thr Ile Ala Val Leu Tyr Cys Val His Gln Arg Ile Asp Val Lys Asp				
225	85 90 95				
226	acc aag gag gcc ctg gac aag atc gag gag gag cag aac aag tcc aag				336
227	Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys				
228	100 105 110				
229	aag aag gcc cag cag gcc gcc gcc gac acc ggc aac aac tcc cag gtg				384
230	Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly Asn Asn Ser Gln Val				
231	115 120 125				
232	tcc cag aac tac ccc atc gtg cag aac ctg cag ggc cag atg gtg cac				432
233	Ser Gln Asn Tyr Pro Ile Val Gln Asn Leu Gln Gly Gln Met Val His				
234	130 135 140				
235	cag gcc atc tcc ccc cgc acc ctg aac gcc tgg gtg aag gtg gtg gag				480
236	Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu				
237	145 150 155 160				
238	gag aag gcc ttc tcc ccc gaa gtc atc ccc atg ttc tcc gcc ctg tcc				528
239	Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser				
240	165 170 175				
241	gag ggc gcc acc ccc cag gac ctg aac acc atg ctg aac acc gtg ggc				576
242	Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly				
243	180 185 190				
244	ggc cac cag gcc gcc atg cag atg ctg aag gag acc atc aac gag gag				624

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VERIFICATION SUMMARY
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Line	? Error/Warning	Original Text
127	W Line data has been corrected	Pro Ser Ser Gln *
302	W Line data has been corrected	Pro Ser Ser Gln *
570	W Line data has been corrected	Asp Asp Cys Val Ala Ser Arg Gln Asp Glu A
898	W Line data has been corrected	Asp Asp Cys Val Ala Ser Arg Gln Asp Glu A
1228	W Line data has been corrected	Asp Asp Cys Val Ala Ser Arg Gln Asp Glu A

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CORRECTION SUMMARY
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Line	Original Text	Corrected Data
127	Pro Ser Ser Gln *	Pro Ser Ser Gln
302	Pro Ser Ser Gln *	Pro Ser Ser Gln
570	Asp Asp Cys Val Ala Ser Arg Gln Asp Glu A	Asp Asp Cys Val Ala Ser Arg Gln Asp Glu A
898	Asp Asp Cys Val Ala Ser Arg Gln Asp Glu A	Asp Asp Cys Val Ala Ser Arg Gln Asp Glu A
1228	Asp Asp Cys Val Ala Ser Arg Gln Asp Glu A	Asp Asp Cys Val Ala Ser Arg Gln Asp Glu A